

SYR-EPHA2-5001-C1.ST25
SEQUENCE LISTING

<110> Syrrx, Inc.
<120> CRYSTALLIZATION OF EPHRIN RECEPTOR A2
<130> SYR-EPHA2-5001-C1
<140> Not Yet Assigned
<141> 2003-06-20
<150> 60/390,356
<151> 2002-06-21
<160> 3
<170> PatentIn version 3.1
<210> 1
<211> 976
<212> PRT
<213> Homo sapiens

<220>
<221> Amino acid sequence for full length human wild type EPHA2
<222> (1)..(976)
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<220>
<221> Amino acid sequence for full length human wild type EPHA2
<222> (1)..(976)
<223> SEQ. ID. No. 1 encodes for residues 596-900

<300>
<308> GenBank Accession No. M59371
<309> 1994-11-21
<313> (1)..(976)

<400> 1

Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys
1 5 10 15

Ala Leu Ala Ala Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu
20 25 30

Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr
35 40 45

Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile
50 55 60

Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp
65 70 75 80

Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Asn Asn Phe
85 90 95

SYR-EPHA2-5001-C1.ST25

Glu Leu Asn Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Ala
100 105 110

Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu
115 120 125

Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr
130 135 140

Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His
145 150 155 160

Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys
165 170 175

Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu
180 185 190

Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu
195 200 205

Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala
210 215 220

Thr Val Ala Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly
225 230 235 240

Glu Glu Pro Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro
245 250 255

Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala
260 265 270

Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser
275 280 285

Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala
290 295 300

Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro
305 310 315 320

Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr
325 330 335

Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln
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SYR-EPHA2-5001-C1.ST25
340 345 350

Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln
355 360 365

Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg
370 375 380

Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser
385 390 395 400

Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn
405 410 415

Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val
420 425 430

Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser
435 440 445

Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser
450 455 460

Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn
465 470 475 480

Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp
485 490 495

Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln
500 505 510

Glut Gly Gln Gly Ala Gly Ser Lys Val His Glu Phe Gln Thr Leu Ser
515 520 525

Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly
530 535 540

Val Val Leu Leu Leu Val Leu Ala Gly Val Gly Phe Phe Ile His Arg
545 550 555 560

Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe
565 570 575

Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His
580 585 590

SYR-EPHA2-5001-C1.ST25

Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile
 595 600 605

His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe
 610 615 620

Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu
 625 630 635 640

Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln
 645 650 655

Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His
 660 665 670

His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met
 675 680 685

Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu
 690 695 700

Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu
 705 710 715 720

Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val
 725 730 735

His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val
 740 745 750

Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro
 755 760 765

Glu Ala Thr Tyr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr
 770 775 780

Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val
 785 790 795 800

Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg
 805 810 815

Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
 820 825 830

Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln
 835 840 845

SYR-EPHA2-5001-C1.ST25

Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe
 850 855 860

Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser
 865 870 875 880

Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro
 885 890 895

Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp
 900 905 910

Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala
 915 920 925

Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile
 930 935 940

Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr
 945 950 955 960

Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
 965 970 975

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<211> 915

<212> DNA

<213> Homo sapiens

<220>

<221> Human cDNA sequence encoding residues 596-900 of EPHA2

<222> (1)..(915)

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cagaaggta	tcggagcagg	agagttggg	gaggtgtaca	agggcatgct	gaagacatcc	120
tcgggaaaga	aggaggtgcc	ggtggccatc	aagacgctga	aagccggcta	cacagagaag	180
cagcgagtgg	acttcctcgg	cgaggccggc	atcatgggcc	agttcagcca	ccacaacatc	240
atccgcctag	agggcgtcat	ctccaaatac	aagcccattga	tgatcatcac	tgagtacatg	300
gagaatgggg	ccctggacaa	gttccttcgg	gagaaggatg	gcgagttcag	cgtgctgcag	360
ctgggtggca	tgctgcgggg	catcgcagct	ggcatgaagt	acctggccaa	catgaactat	420
gtgcaccgtg	acctggctgc	ccgcaacatc	ctcgtcaaca	gcaacctgg	ctgcaagg	480
tctgactttg	gcctgtcccc	cgtgctggag	gacgaccccg	aggccaccta	caccaccagt	540
ggcggcaaga	tccccatccg	ctggaccgccc	ccggaggcca	tttccttaccg	gaagttcacc	600

SYR-EPHA2-5001-C1.ST25

tctgccagcg acgtgtggag ctttggcatt gtcatgtggg aggtgatgac ctatggcag 660
cggccctact gggagttgtc caaccacgag gtgatgaaag ccatcaatga tggcttccgg 720
ctccccacac ccatggactg cccctccgccc atctaccagc tcatgatgca gtgctggcag 780
caggagcgtg cccgcccggcc caagttcgct gacatcgta gcatcctgga caagctcatt 840
cgtgcccctg actccctcaa gaccctggct gacttgacc cccgcgtgtc tatccggctc 900
cccagcacga gcggc 915

<210> 3
<211> 333

<212> PRT

<213> Homo sapiens

<220>

<221> Amino acid sequence for residues 596-900 of EPHA2 with a cleavable (rTev) N-terminal 6x-histidine tag

<222> (1)..(333)

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<221> Cleavable (rTev) N-terminal 6x-histidine tag

<222> (1)..(28)

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Met Ser Tyr Tyr His His His His Asp Tyr Asp Ile Pro Thr
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Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Gly Ser Asp Pro Asn Gln
20 25 30

Ala Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg
35 40 45

Gln Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met
50 55 60

Leu Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr
65 70 75 80

Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu
85 90 95

Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu
100 105 110

Gly Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met
115 120 125

SYR-EPHA2-5001-C1.ST25

Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe
130 135 140

Ser Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met
145 150 155 160

Lys Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg
165 170 175

Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly
180 185 190

Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser
195 200 205

Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr
210 215 220

Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met
225 230 235 240

Trp Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn
245 250 255

His Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro
260 265 270

Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln
275 280 285

Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu
290 295 300

Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe
305 310 315 320

Asp Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly
325 330